

Figure 1A

1	CGGACGCGTGGGCGCGCAGCGCTGGTGACCTGATCCTGGACCGTGCCCCGACCGCGCG	60
61	CGCCGGTGC CC CAGATGCTGCC CC CAGCGCGCAGCGGCTGCTCTTCATCCTGGACGGCGCG	120
1	M H A Q P Q R L H F I L D G A D	16
121	ACGAGCTGCC CC GCTGGGGGCCCGAGGCGCGCCCTGCACAGACCCCTTCGAGGCGG	180
17	E L P A L G G P E A A P C T D P F E A A	36
181	CGAGCGGCCGCGGGTCTAGGGGGCTGCTGACTAAGGGCTGCTGCCACGGCCCTCC	240
37	S G A R V H G G H S K A L H P T A L L	56
241	TGCTGGTGACCA C CGCGCGCCGCCGCCGGAGGCTGAGGGCCGCCGTGTTCCC G	300
57	H V T T R A A A P G R H Q G R L C S P Q	76
301	AGTGCGCCAGGTGCGCGCTTCCGACAAGGACAAGAAAGAAGTATTCTACAAGTCT	360
77	C A E V R G F S D K D K K K Y F Y K F F	96
361	TCCGGGATGA G AGAGGAGGGCGAGCGCGCTACCGCTTCTGAGGGAGAACGAGACCGCTG	420
97	R D E R R A E R A Y R F V K E N E T H F	116
421	TCGGCTGTGCTTCGCTGCCCTCGTGTGCTGGATCGTGCGACCGTGTGGCCAGCACG	480
117	A L C F V P F V C W I V C T V H R Q Q L	136
481	TGGAGCTCGTGGGACCTCTCGCGCACGTCCAAGAACCAACGTCAGTGTACCTGCTT	540
137	E L G R D L S R T S K T T T S V Y H L F	156
541	TCATCACAGCTTCTGAGCTCGGCTCCGGTAGGCCAGGGGCCGGTTGCAGGGCGACC	600
157	I T S V L S S A P V A D G P R L Q G D H	176
601	TGCGCAATCTGTGCGCCCTGGCCCGAGGGCGTCTCGGACGCAGGGCGAGTTGCG	660
177	R N H C R H A R E G V L G R R A Q F A E	196
661	AGAAGGAAC T GGAGCAACTGGAGCTTCGTTGGCTCCAAAGTGCAGACGCTGTTCTCAGCA	720
197	K E H E Q L E L R G S K V Q T L F L S K	216
721	AAAAGGAGCTGGCGGGCGTGTGGAGACAGAGGTCACCTACCGTTCATCGACCGAGCT	780
217	K E L P G V L E T E V T Y Q F I D Q S F	236
781	TCCAGGAGTTCCTCGCGGCACTCTCCTACCTGCTGGAGACGCCAGGGGTGCCAGGGCG	840
237	Q E F L A A L S Y L H E D G G V P R T A	256
841	CGGCTGGCGGGTGGGACACTCCTGCGTGGGGACGCCAGCCGACAGCCACTTGGTGC	900
257	A G G V G T L H R G D A Q P H S H L V L	276

Figure 1B

901	TCACCA CGC GCTT CCT CTT CGG ACT GCT GAG CGG AGCGG AT GCG GAC AT CGA CGCC	960
277	T T R F L F G H L S A E R M R D I E R H	296
961	ACTT CGG CTG CAT GTG TT CAG AGCGT GTG AGG CAG GAG GGG CCT GCG GTGGG TGAGG GAC	1020
297	F G C M V S E R V K Q E A L R W V Q G Q	316
1021	AGGG ACAGGG CTG CCCC GGAGT GCG ACCA GAGGT GAGC GAGGG GGG CAA AGGG CTG AGG	1080
317	G Q G C P G V A P E V T E G A K G L E D	336
1081	ACACCG AAG AGCC AAG GAGG AGGG AGGG AGGG AGGG CCA ACT ACCA CTG GAG TTGC	1140
337	T E E P E E E E G E E P N Y P L E L H	356
1141	TGT ACT GCG CTG TAC GAG ACC GAG GAGG AGCG CTT TGCG CCA AGG CCT GTG CGG TTCC	1200
357	Y G H Y E T Q E D A F V R Q A L C R F P	376
1201	CGG AGC TGG CG CTG CAG CG AGT GCG CT TCG CC GAT GG ACC TG CT GAG CTA CT	1260
377	E L A L Q R V R F C R M D V A V L S Y C	396
1261	GCG T GAG GT GCT GCCC CT GCT GG A CAG G C A C T G C G G C T G A T C G C T G C A G A T T G G T G C T G	1320
397	V R C C P A G Q A L R E I S C R L V A A	416
1321	CGC AGG AGA GAG AAG AAG AGG C T G G G A A G C G G C T C C A G G C C A G G C T G G G C G G C A	1380
417	Q E K K K S H G K R L Q A S L G G G S	436
1381	GTT CT CAAG G C A C C A A A A C A C T G C C A G C T C C C T T C T C A T C C A C T C T T C A G G C A A	1440
437	S Q G T T K Q H P A S L L H P L F Q A M	456
1441	TG ACT GAC C C A C T G C C A T G C A G C A G C C T C A C G C T G F C C C A C T G C A A A C T C C C T G A C G	1500
457	T D P L G H S S L T L S H C K L P D A	476
1501	CGG T CT GCG GAG A C T T C T GAG G C C T GAG G C A G C C C C G C A C T G A C G G A G G C T G G G C	1560
477	V C R D L S E A T R A A P A L T E G H	496
1561	T C C T C C A A C A C G G C T C A G T GAG G C G G A C T G C G T A T G C T G A C T G A G G G C C T A G C C T G G C	1620
497	L H N R L S E A G L R M H S E G L A W P	516
1621	C G C A G T G C A G G G T C C A G A C G G T C A G G G T A C A G C T G C C T G A C C C C A G G G A G G G T C C A G T	1680
517	Q G R V Q T V R V Q L P D P Q R G L Q Y	536
1681	A C C T G G T G G G T A T G C T T C G G C A G A G C C C C G C C T G A C C A C C T G G A T C T C A G C G G C T G C C	1740
537	H V G M E R Q S P A H T T L D H S G C Q	556
1741	A A C T G C C C G C C C C A T G G T G A C C T A C C T G T G C A G T C C T G C A G C A C C A G G G A T G C C G C C	1800
557	H P A F M V T Y L C A V I Q H Q G G G L	576

1000 900 800 700 600 500 400 300 200 100

Figure 1C

1801	TGCAGACCCCTCAGTCIGGCCCTGTGGAGCTGAGCGAGCAGTCACTACAGGAGCTTCAGG	1860
577	Q T S A S V E S E Q S L Q E Q A	596
1861	CTGTGAAGAGAGCAAAGCCGGATCTGGTCATCACACACCCAGCGCTGGACGGCCACCCAC	1920
597	V K R A K P D V I T H P A L D G H P Q	616
1921	AACCTCCCAAGGAACTCATCTCGACCTCTGAGGCTCTGGTGGCCAGAGCAGGGTGGAAAG	1980
617	P P K E L I S T F	625
1981	ACCCTAGTCAAAGTCCCTGTGGAGAGAACGGCCCATTCCAAGGGCAGGAGGATATTGCTC	2040
2041	TCGGCCTTTGGGAAACTTGTGAGCCGAGAGGCCGCAGACAGGCATGTGGAGGCCAGAC	2100
2101	ACGGCACCCCTGCCCCGTCCAGGA CAGGCCAGGACCTGCCCCCTCTCCACACCTGGGT	2160
2161	ACCCCTCTCCCCAGCCCCACCACACTCCACCCACCTCTCTGAGACCCCTCCAG	2220
2221	CCATTCCCCTTGAAAACACCCCCCGAGCCCAAGCCACAATAATGACAGCGAGAGCTCAA	2280
2281	TTAACTAAGCACCTACCTGGCGGCAGAATAACCTTCACTGCCTGATCCCCATCTGCAGT	2340
2341	GTGGCCCAACAGCCCCAGAACTATGCCACATAGACTGGAGGTAGGCAGTTACCGTCC	2400
2401	CTCCCTGTTAGGAATGAGACCATCCCTGAGGCTATGGCCAGGCCACAGCGTCCAGTG	2460
2461	TCTGAGATCTTGGAGGGAGACTAGGGCAGGTGGAGACAGOGCAGAACCCCCGTGCTG	2520
2521	GGTGGGAAGCATGACCACATGGTGGGTGAGCAGCCCCATGCACTGACGGTAAATTCCCC	2580
2581	TGTGGACTCATTCCTGTTGGTTCTATTACACCTGGCCAGGCAGTGGTACAATACAGGTCG	2640
2641	GTCACAAAAAAAAAAAAAAAAAAAAAA 2689	

2000 1950 1900 1850 1800 1750 1700 1650 1600 1550 1500 1450 1400 1350 1300 1250 1200 1150 1100 1050 1000 950 900 850 800 750 700 650 600 550 500 450 400 350 300 250 200 150 100 50

Figure 2B

HLRRSII
caspase_recruitment_protein
cryopyrin
Nucleotide_Binding_site

	601	650
(203)	PLGSKVQDPLSKKE[PGV]EDVLTIFDID[SPQEELAISYLDLGGV]	
(595)	GILGRATSTFMKG---[DLSHPIPLSFHHLFQEEFANSI[LEDEW]	
(491)	SLGRKADVEETV[EN]VQCEGDDC[DTYSFIE]LFOE[AMYVLPDEK]	
(446)	EVNSPSDPRIFPQGD-[R]LGRV[EGCFYSFIHLFSQ[ER]FVYTFLE]	
	651	700
(253)	P[IV]Y[CS]-----[NGV[AGGAQPHS]FVLTAIFLGILIA[PR]AD	
(642)	-----[SRGKHSNCIIDDEKTE[RTAYGNGICFGAS]TTFI[GLI]G[GP]RS	
(540)	CGT[IV]SRLKLPSRQDV[ELLENYERREKGLI]F[AF]LFGLVNC[ERTSY]	
(495)	EDRGHTW[DIG]---[EVQLLSG[V]PQRNPFLIO[GYY]SFGLA[TRR]E	
	701	750
(293)	MES[HF]GOMPSR[KA]QEV[L]RNWV[Q]QQCCPGVAP[EVT]E[AKC]L[Q]E[EE]D	
(686)	M[DN]I[PR]I[S]C[GRNL]Q[K]V[P]-----[Q]LLQ[EF]S	
(590)	LEDK[Q]C[SD]Q[SD]L[EL]L[EV]K-----[A]K[A]LQ[Q]C[Q]	
(541)	LEATE[G]C[SD]P[K]Q[EL]L[C]D[I]C-----[K]G[CH]T[TD]Q	
	751	800
(343)	EEEGEEP[N]P[ELLY]LCY[ET]O[EV]R[ALCRFPPE]L[LR]V[R]F[RD]W[V]	
(716)	-----[LES]H[CL]Y[ET]O[EV]R[ALCRFPPE]L[LR]V[R]F[RD]W[V]	
(626)	[ELLY]LCY[ET]O[EV]R[ALCRFPPE]L[LR]V[R]F[RD]W[V]-----[R]STRM[H]Y	
(576)	EL[G]C[GL]Y[ET]O[EV]R[ALCRFPPE]L[LR]V[R]F[RD]W[V]-----[L]LAW[D]V[P]	
	801	850
(393)	I[SY]W[RC]SPAC[AR]L[SC]R[VA]R[CE]KK[K]S[GR]L[AS]L[EG]S[Q]	
(754)	C[FG]C[PS]H[B]V[K]L[Q]L[EG]C[H]R[ST]W[SP]S[V]W[L]F[W]P[PT]E[Y]W[O]L[F]	
(664)	S[SF]C[TC]R[CV]P[LS]G[FL]H[NE]K[ES]E[E]E[K]C[PS]L[MC]C[LE]S[SS]M[A]	
(612)	S[SF]C[TC]R[CV]P[LS]G[FL]H[NE]K[ES]E[E]E[K]C[PS]L[MC]C[LE]S[SS]M[A]	
	851	900
(439)	-----	
(803)	-----	
(714)	CSHG[EV]N[SH]-----[LT]	
(662)	DLC[G]FC[SN]KDLMLG[LA]IN[DS]FLS[AS]LV[FL]C[Q]IAS[UT]CH[Q]R[V]VF[K]N[ES]	
	901	950
(439)	-----[CT]K[Q]D[AS]L[EE]T[FO]R[T]I[Q]L[EE]H[ST]	
(803)	-----[V]K[V]R[ML][EL]L[Q]S[NS]I[SA]K[V]C[FL][E]R[LE]I[TR]	
(725)	S[SF]C[R]GL[F]V[TS]QS[Q]-----[EL]L[DS]N[SI]-----[C]H[MR]V[CT]C[Q]H[G]P[TR]	
(712)	PA[DA]HR[N]L[CA]L[H]K[V]T[YL]TLQ[N]D[CD]I[ME]P[AC]C[EL]H[CN]R[Y]	
	951	1000
(468)	L[SH]K[ML]P[D]A[P]S[AL]R[A]P[A]L[T]E[L]L[IR]R[SE]A[G]L[IS]E[G]A[M]Q	
(844)	U[AG]C[G]T[A]B[Q]C[Q]L[Q]A[G]L[R]A[N]C[Q]L[L]E[L]L[SP]V[ND]A[G]H[Q]C[G]R[E]S	
(775)	D[PG]C[G]T[SH]C[Q]L[Q]A[G]L[R]A[N]C[Q]L[L]E[L]L[SP]V[ND]A[G]H[Q]C[G]R[E]S	
(762)	E[X]S[SP]T[Q]O[W]A[Q]L[Q]A[L]T[C]Q[N]L[Q]D[EL]E[Q]G[Q]W[Y]T[LT]R[SH]K	
	1001	1050
(518)	C[Q]V[CF]V[Q]LPPD[Q]-R[G]L[Y]V[G]M[R]A[SE]A[L]T[L]L[DD]G[CC]P[A]R[M]V[TC]	
(894)	C[Q]L[RC]L[V]S[Q]L[Q]S[CC]Q[DL]A[V]S[Q]P[SL]K[EL]D[Q]N[LP]C[G]P[V]G[VC]R[Q]	
(825)	C[Q]L[RC]L[V]S[Q]L[Q]S[CC]Q[DL]A[V]S[Q]P[SL]K[EL]D[Q]N[LP]C[G]P[V]G[VC]R[Q]	
(812)	C[Q]L[RC]L[V]S[Q]L[Q]S[CC]Q[DL]A[V]S[Q]P[SL]K[EL]D[Q]N[LP]C[G]P[V]G[VC]R[Q]	
	1051	1100
(567)	A[V]L[A]Q[Q]C[L]Q[L]A[L]S[V]E[L]G[S]L[Q]L[Q]E[V]K[A]R[E]L[L]I[T]P[Q]D[G]HQ	
(944)	E[G]L[R]H[P]C[K]M[I]R[L]Q[D]Q[TC]S[D]P[M]P[E]T[R]D[E]K[E]A[L]L[L]I[S]P[R]K[P]M[T]	
(875)	E[K]A[N]G[C]C[L]Q[D]Q[TC]S[D]P[M]P[E]T[R]D[E]K[E]A[L]L[L]I[S]P[R]K[P]M[T]	
(862)	E[G]L[R]H[P]C[K]LQ[D]Q[TC]S[D]P[M]P[E]T[R]D[E]K[E]A[L]L[L]I[S]P[R]K[P]M[T]	
	1101	1150
(617)	H[P]K[L]I[ST]F-----	
(994)	K[EG]D[G]T[G]E[S]N[T]S[Q]S[Q]P[Q]S[Q]P[Q]S[Q]P[Q]S[Q]P[Q]S[Q]P[Q]S[Q]P[Q]S[Q]P[Q]	
(925)	K[EG]D[G]T[G]E[S]N[T]S[Q]S[Q]P[Q]S[Q]P[Q]S[Q]P[Q]S[Q]P[Q]S[Q]P[Q]S[Q]P[Q]S[Q]P[Q]	
(912)	K[EG]D[G]T[G]E[S]N[T]S[Q]S[Q]P[Q]S[Q]P[Q]S[Q]P[Q]S[Q]P[Q]S[Q]P[Q]S[Q]P[Q]S[Q]P[Q]	
	1151	1200
(626)	-----	
(1044)	N[E]S[S]P[Q]N[V]P[Q]E[L]C[Q]P[Q]P[A]S[Q]C[B]L[H]T[R]P[G]T[D]E[G]P[G]P[G]V[TC]	
(975)	G[Q]-----[L]D[G]G[V]P[C]P[Q]-----[S]C[Q]L[N]G[Q]S[Q]L[R]K[Q]	
(961)	G[Q]-----[L]D[G]G[V]P[C]P[Q]-----[S]C[Q]L[N]G[Q]S[Q]L[R]K[Q]	

Figure 2C

	1201	1250
HLRRSII	(626)	
caspase_recruitment_protein	(1094)	ENLYRNPDPVAGSFRWPNTGLOVVREAVTVEIEFCVWDQFLGEINPQR
cryopyrin	(1022)	ASP-DIVVPSW-
Nucleotide_Binding_site	(1008)	AKKGLIDTEKHHHPAERPS3HD
	1251	1300
HLRRSII	(626)	
caspase_recruitment_protein	(1144)	SKMVAQGPLLDIKAEPGAVEAVHLPHFVALQQGHVDTSLFCVAHFKEGML
cryopyrin	(1035)	-
Nucleotide_Binding_site	(1034)	-
	1301	1350
HLRRSII	(626)	
caspase_recruitment_protein	(1194)	LEKPARVELHHIVLENPSFSPLGVLLKNIHNAALRFIPVTSVVLLYHRLHP
cryopyrin	(1035)	-
Nucleotide_Binding_site	(1034)	-
	1351	1400
HLRRSII	(626)	
caspase_recruitment_protein	(1244)	EEVTFHLYLIPSDCSIRKELELCYRSPGEDQLFSEFYVGHLSGIRLQVK
cryopyrin	(1035)	-
Nucleotide_Binding_site	(1034)	-
	1401	1450
HLRRSII	(626)	
caspase_recruitment_protein	(1294)	DKKDETLVWEALVKPGDLMPTATTLIPPIACIAVPSPLADPQLLHFVDQYRE
cryopyrin	(1035)	-
Nucleotide_Binding_site	(1034)	-
	1451	1500
HLRRSII	(626)	
caspase_recruitment_protein	(1344)	QLIARVTSVEVVLSDLHGQVLSQEYQYERVLAENTRPSQMRKLFSLSQWD
cryopyrin	(1035)	-
Nucleotide_Binding_site	(1034)	-
	1501	1536
HLRRSII	(626)	
caspase_recruitment_protein	(1394)	RKCKDGLYQALKETHPHLIMELWEKGSKGLLPLSS
cryopyrin	(1035)	-
Nucleotide_Binding_site	(1034)	-

D0066 NP

Figure 3

Figure 3

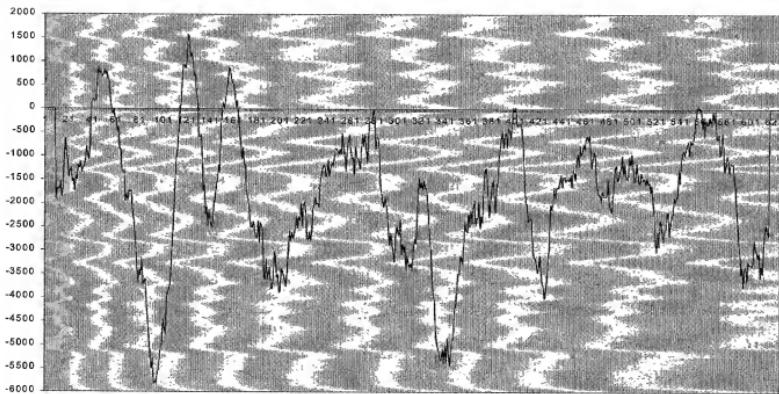
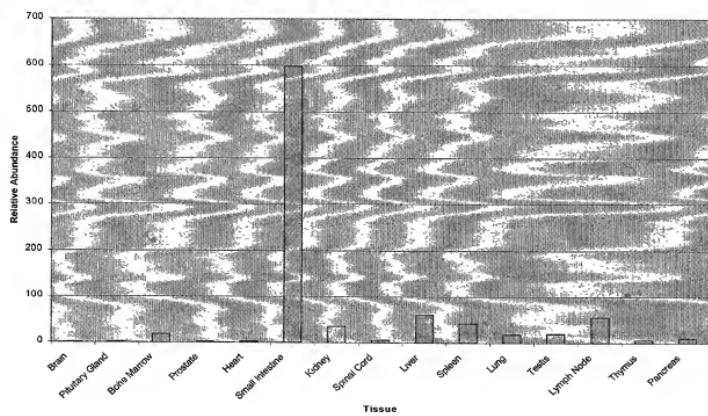


Figure 4



D0066 NP

Figure 5.

Protein	Genbank ID	Identities	Similarities
human caspase recruitment protein 7	gi 10198209	36.3%	44.0%
human nucleotide binding site protein	gi 10198207	35.0%	42.2%
human cryopyrin protein	gi 17027237	35.7%	46.0%